CTCATCATCGCCGGACTGCTGATCGTTGGCGGGCGTGACGGAGGCCGCCGGCATGCGCCGCTCATGTTCGAGGAGTCCGACACG	GGCAGGCGGTCCAACCGACCAGGTCACCGAATGCCAAAGTTTTGCGCGAATTGGGGTCCACCTGGTATGCGGTTTTGGGT	CCACCCTTCGGAGTTATGTACTGCATCAAGTGTGAATGTGTGGCGCATACCCAAGAAGCGGCGCATCGTTGCACGCGTCCACGCAAT	ATCADADAGGAGTGCCGCCGGCCGADATGCGATGATCCCATCTCGTTGCCGGADADATGCTGCAGAGACCTGTCCCGGCGATCGADAACGAT	ACGGATGTAGCCTTGGATGTGCCCGTGCCCAATGAAGAGGGCGCAACATGAAACATTACGCTGCGTTGCTAACGGGCCGCACCTCC T D V P N E E E E R N M K H Y A A L L T G R T S	TATITICCTCAAGGGTGAAATGAAGTCCATGTACACCTACAATCCGCAGAATCTGGTGGCCACCGCCGTTTCCTGTTCCAAAG Y F L K G E E M K S M Y T T Y N P Q N V V A T A R F L F H K	AAGAATCTATACTACTCCTTCTACACCTCACGAATCGGTCGTCCGCGGTGCATTCGTTGATGATGCGGGTGTAATCCTGGAG K N L Y Y S F Y T S S R I G R P R A I Q F V D D A G V I L E	GAGCATCAACTGGAGCACCTTGGCGGCACTCTCAGTGTCTAGAATGCCACGGGCAAGATCTGA
₩ 860	SE C	EGA	DGAT	IGAA E	3TAC Y	SCGA R	CTC
Ę J	E E	GTG	D GA	CAA	CATC	ATCC S	CAC1
D CT	CAC T	A ×	C	Ď ď	GTC	CTC	ဗ္ဗဗ္ဗ
	V	I	KE	CGT V	ξ.Α ×	T.	GGC A
TGA	CAG	S C	₽ SGG	IGCC P	ÆAT M	rcra Y	CTT
130	GAC	TGT >	<u> </u>	ATG.	AGG)	CCT	CCAC
SGAC	2 Z	ŢŢ		TGG O	GTG E	ACT	AGA T
3000	D Z	GAG	PAG	CCT	998	ACT	TGG
ATCC	555	E .	A CO	TAG	OF.	TAT.	AAC I
ATC	AGG(A Y	SATC	rrcc F L	ATC I	ATC
77	0 0	S a	ATC	A H	TAT.	AAG!	GAG(

361 121

451

541 181

631

721

271 91

SR1

TM

GAGGACGCCGCACTGGAGCCAAGCGAAAAAACCAGCCATAGAGAACAAGCCCCCATCCTGCGCCACCTGAGCCAACTGAGCCACCTG

ATGGCCAACAAGTTGAAATTGAAGCCATGGAATGGGCCACGGCACAGTACCGCTCCTGGAAAGGAGCTGCTGCCACAGG M A N K L R K S N A I E W A T A T G T V P L L E R S C C H S

31

91

181

FIGURE 1

VYANAT

811 271

Т			CRI					PUAS	Sequences
1 ATGGCCAACAAGCTGAAGGAAATCGAATGGGCCACGGCCACCGGCACAGTACCGCTCCTGGAAAGGAGCTGCCACAGCCACAGCCACAGCCACAGCCACAGCCACAGCCACAGCCACAGCCACAGCCACAGCCACAGCCACAGCCACAGCCAAAACCAGCCATAGAAACCAGCCCCATCCTGCGCCCACCTGAGCCAACTGAGCCACCTGAGCCAACTGAGCCACCTGAAAACCAGCCATAGAAAAAAAA	TCTCATCATCGCGGGACTGCTGGCGGGGGGGGGGGGCCGCGGCATGCGCCGCTCATGTTCGAGGGTCCGACACG 1 1 1 1 1 1 1 1 1 1	1 GGCAGGCGGTCCAACCGACCACCGAATGCCAGTTTGGCAAAGTTTTGCGCGAATTGGGGTCCACCTGGTATGCGCATTTGGGT	1 CCACCCTTCGGAGTTATGTACTGCATCAGATGTGCGCATACCCAAGAAGCGGCGCATCGTTGCACGCGTCCAGTGTCGCAAT		1 ACGGATGTAGCCTTGGATGTGCCCGTGCCCAATGAAGAGGGGGAACATGAAAACATTACGCTGCGTTGCTAACGGGCCGCACCTCC 1 T D V A L D V P V P N E E E E R N M K H Y A A L L T G R T S 1 T D V A L D V P V P N E E E E R N M K H Y A A L L T G R T S		1 AAGAATCTATACTACTTCTACACCTCATCGCAATCGGTCCCCGTGCCATTCAATTCGTTGATGAGGGGGTGTAATCCTGGAG 1 K N L Y Y S F Y T S S R I G R P R A I Q F V D D A G V I L E	1 GAGCATCAACTGGAGACCACCTTGGCGGCACTCTCAGTCTATCAGAATGCCACGGGCAAGATGGGCGGGGGGGG	$egin{array}{cccccccccccccccccccccccccccccccccccc$
о м	181	271 91	361	451	541 181	631	721	811	301

FIGURE 2

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	ΑT		.CR1:W->A				<u>PUAS</u> <u>Sequences</u>				
	AAGGAGCTGCTGCCACAGC RSCCHS GAGCCAACTGAGCCACCTG	S Q L S H L GTTCGAGGAGTCCGACACG F E E S D T		TCCCGGCGATCGAAACGAT	3CTAACGGGCCGCACCTCC L T G R T S CGTTTCCTGTTCCACAAG	R F L F H K TGCGGGTGTAATCCTGGAG A G V I L E	G S R V P L CTCTAA CTCTAA L STOP	ľ			•
	CACGGCCACGGCACAGTACCGCTCCTGGA T A T G T V P L L E TAGAGAACCCCCCATCCTGGGCGCT	KEUAFILKHI GACGGAGGCCGCCGCATCCGCCGCTCATI TEGRRHAPLM	TGGCAAAGTTTTGCGCGAATTGGGGTCCAC G K V L R E L G S T GCGCATACCCAAGAAGCGGCGCATCGTTGC A I P K K R R I V A	CICGIIGCCCGGAAAIGCIGCAAGACCIG: S L P G K C C K I C	AGAGCGCAACATGAAACATTACGCTGCGTTK E R N M K H Y A A L TTACAATCCGCAGAATCTGGTGGCCACCGCC	Y N P Q N V V A T A ICGICCGCGGCCATTCAATTCGTTGATGAI R P R A I Q F V D D	TATCAGAATGCCACGGCAAGATGGCCGC Y A N A T G K I G R ATTGACAAACTACCTACAGAGATTTAAAG I G N T T Y R D L K	FIGURE 3			 * , .
	ATGGCCAACAAGCTGAGAAATGGCCATGAATGGGCCACGGCCACGGCACAGTACCGCTCCTGGAAAGGAGCTGCTGCCACAGC M A N K L R K S N A I E W A T A T G T V P L L E R S C C H S GAGGACGCCGCACTGGAGCCCAAGCGAAAAACCAGCCATAGAGAACAAAGCCCCCATCCTGGGCCACTGAGCCAACTGAGCCACTGA	CTCATCATCGCCGGACTGCTGATCGTCTTGGCGGCGTGACGGAGGGCCGCCGCCGCCGCCGCCGCTCATGTTCGAGGAGTCCGACGCCGCCGCCGCCGCCGCCGCCGCTCATGTTCGAGGAGTCCGACACG	GGCAGGCGGTCCAACCGACCGGGTCACCGGATTGGCCAATTGCGCGAATTGGGGTCCACCTGGTATGGGATTTGGGT G R R S N R P A V T E C Q F G K V L R E L G S T W Y A D L G CCACCCTTGGGAGTTATGTACTGCATCAAGTGTGAATGTGTGCGCATACCCAAGAAGCGGCGCCATCGTTGCACGCGTCCAGTGTGCAAT P F G V M Y C I K C E C V A I P K K R I V A R V Q C R N)	AICAAAAAGGAGIGCCGGCCGAAAIGCGAIGAICCCAICICGIIGCCGGAAAAIGCIGCAAGACCIGICCCGGCGAICGAAACGAI I K N E C P P A K C D D P I S L P G K C C K T C P G D R N D	ACGATGTAGCCTTGGATGTGCCCGTGCCCAATGAAGAGGAAGAGCGCAACATGAAACATTACGCTGCGTTGCTAACGGGCCGCACCTCC T D V A L D V P V P N E E E R N M K H Y A A L L T G R T S * * * * * * * * * * * * * * * * * *	YFLKGEEMKSMYTTYNPQNVATARFLFHK AAGAATCTATACTACTCTCTCATCGCGAICGGTCGTCGTCGCGTGTCAATTCGTTGATGATGAGGGGGTGTAATCCTGGAG KNLYYSFYTSSRIGRPRATC	GAGCATCAACTGGAGACCACCTTGGCGGCACTCTCAGTGTCAGAATGCCACGGGCAAGATGGGCGGGGCTCGAGGGTACCTCTA E H Q L E T L A G T L S V Y A N A T G K I G R G S R V P L GAGGATCTTTGTGAAGGAACCTTACTTCTGTGGTGTGACATAATTGGACAAACTACCTAC	FIG	4.	, .	
	1 16 17	181	271 91 361 121	451	541 181 631	211 721 241	811 271 901 301				•

44	ATGGCCAACAAGAGGAAATGGAAGGCCATGGAATGGGCCACGGCCACGGTACCGCTCCTGGAAAGGAGCTGCTGCCACAGC M A N K L R K S N A I E W A I A I G I V P L L R R S C C H S	
91	CAGCCATAGAGAACAAGCCCCATCCTGCGCCACCTGAGCCAACTGAGCCCAC S H R E Q A P I L R H L S Q L S H	
181 61	CTCATCATCGCGGGACTGCTGGTTGGCGGGCGTGACGGAGGGCCGCCGGCGCGCTCATGTTCGAGGGGTCCGACACG	
271 91	GGCAGGCGGTCCAACCGACCAGCGACTCACCAAAGTTTTGCGCGAATTGGGGTCCACCTGGTATGCGGATTTGGGT G R R S N R P A V T E C Q F G K V L R E L G S T W Y A D L G	
361	CCACCCTTCGGAGTTATGTACTGCATGAGAGTGTGCGCATACCCAAGAAGCGGCGCGCATCGTTGCACGCGTCCAGTGTCGCAAT	
451	ATCABABAACGAGTGCCGGCCGAATGATGATCCCATCTCGTTGCCGGAAAATGCTGCAAGACCTGTCCCGGCGATGGAAACGAT	
541 181	ACGGATGTAGCCTTGGATGTGCCCCAATGAAGAGGAAGAAGAACATGAAACATTACGCTGCGTTGCTAACGGGCCGCACCTCC T D V A L D V P V P N E E E E R N M K H Y A A L L T G R T S *	
631 211	TATTICCICAAGGGIGAGGAAIGAAGICCATGIACACCACCACAGAATCIGGIGGCCACCGCCGTITCCIGITCCACAAG Y F L K G E E M K S M Y T I Y N P Q N V V A I A R F L F H K	
721	AAGAATCTATACTACTCCTTCTACACCTCCGCGAATCGGTCCGCGTGCCATTCGTTGATGATGCGGGGTGTAATCCTGGAG K N L Y Y S F Y T S S R I G R P R A I Q F V D D A G V I L E	
811 271	GAGCATCAACTGGAGACCACCTTGGCGGGCACTCTCAGTGTCAGAATGCCACGGGCAAGATCGGCCGCGCGCTCGAGGCAGCGGGGGUAS/PCR E H Q L·E T T L A G T L S V Y A N A T G K I <u>G R G S R N R G</u> PUAS/PCR	
301	CGCATCTTTTACCCATACGATGTTCCTGACTATGCGGGCTATCCCTATCACGGACTATGCACGATCCTATCCATATGACCTTCCA R I F Y P Y D V F D Y A G Y P Y D V P C Y B Y D V P C Y A G S Y P Y D V P C Y A C S Y P Y D V P C Y A C Y A C S Y P Y D V P C Y A C Y A C S Y P Y D V P C Y A C	
991	GATTACGCTGCTCAGTGCGGCGGCGATTATACGGACGACGACGACAAATCA N C G R D Y K D D R S S S S S S S S S S S S S S S S S	

FIGURE 4

Sequence Range: 1 to 222

70 RTLMVGHFDP	o gTLsVygn	TLMVGHFDP	150	VLYTWNDLG				
60 OPKEKDLNETLLI	260 270 280 _iqfvddagvIleEhgLetTLagTLsVyqn _i^i^i^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^	VDLI EHPDPIYDPKEKDLNETLLRTLMVGHFDP	140	.LQMWLWSQTFCE			220	ISECKCSC
50 /DLIEHPDPIYI	260 270 _iqfvddagvIle- _************************************	льгенроргуг	130	KHRLSKKLRR			210	KCAWITIQYPV
40 APSENLPLV	26	_	120	EFYEGLQSK			200	WRCQRRVQQ
30 ХССОНҮЦНІR			110	SGAMPAEIKGL	310 pUAS Vector		190	AAKSMHLTILR
20 IVFLGLRIDQ			100	LDLLLRQKP	310 pU gtiliw>	v- LDLLLR	180	SVPEGMVCK
10 20 30 40 50 60 70 MDHSQCLVTIYALMVFLGLRIDQGGCQHYLHIRPAPSENLPLVDLIEHPDPIYDPKEKDLNETLLRTLMVGHFDP			06	ILPEERLGVEDLGELDLLLRQKPSGAMPAEIKGLEFYEGLQSKKHRLSKKLRRKLQMWLWSQTFCPVLYTWNDLG	300 310 IgrgsRvplEDLcEgtLLLw>	ILPEERLGVEDLGELDLLLR	170	RYVKVGSCYSKRSCSVPEGMVCKAAKSMHLTILRWRCQRRVQQKCAWİTIQYPVISECKCSC
Nog protei	SuperSog P [71]	Nog protei		Nog protei	SuperSog P	Nog protei		Nog protei

FIGURE 5

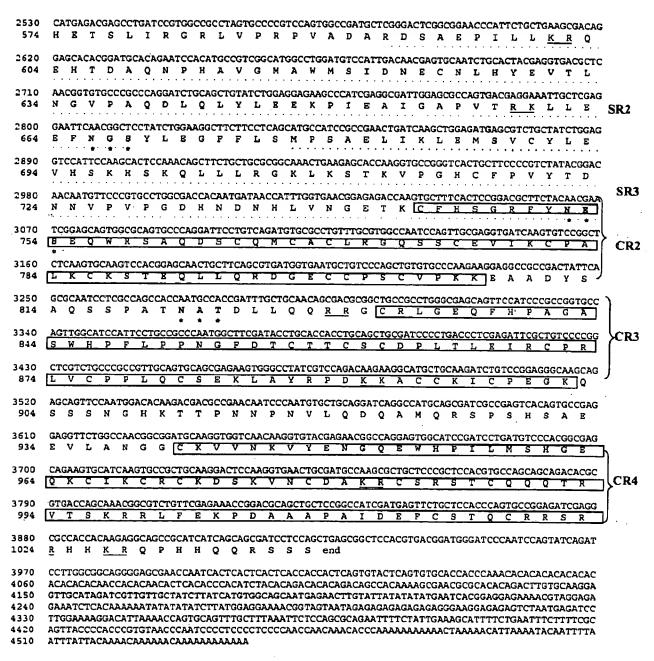


FIGURE 6